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1 **Fabrication of a disposable biosensor for Escherichia Coli O157:H7
detection**
Muhammad-Tahir, Z.; Alocilja, E.C.;
Sensors Journal, IEEE , Volume: 3 , Issue: 4 , Aug. 2003
Pages:345 - 351

[Abstract]   [PDF Full-Text (614 KB)]   **IEEE JNL**

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2 **A novel method of measuring the thickness of hydrated ultrathin
polymer film by the force curve of atomic force microscopy**
Wu, C.C.; Chang, H.C.;
Microtechnologies in Medicine & Biology 2nd Annual International IEEE-EMB
Special Topic Conference on , 2-4 May 2002
Pages:27 - 30

[Abstract]   [PDF Full-Text (436 KB)]   **IEEE CNF**

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1 **A mutual coupling study of circular polarized microstrip antennas witl applications to diversity combining mobile communications**
Ramirez, R.R.; De Flaviis, F.;
Antennas and Propagation Society International Symposium, 2001. IEEE , Volui
3 , 8-13 July 2001
Pages:244 - 247 vol.3

[Abstract] [PDF Full-Text (200 KB)] **IEEE CNF**

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2 **Measurements of solder bump lifetime as a function of underfill matei properties**
Nysaether, J.B.; Lundstrom, P.; Liu, J.;
The First IEEE International Symposium on Polymeric Electronics Packaging
, 26-30 Oct. 1997
Pages:307 - 314

[Abstract] [PDF Full-Text (640 KB)] **IEEE CNF**

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3 **The effect of ring electrodes attachment to a corona gun on control of free ion concentration and back corona for improving powder paint appearance**
Biris, A.S.; Mazumder, M.K.; Sims, R.A.; Yurteri, C.U.; Farmer, S.; Snodgrass, .
Industry Applications, IEEE Transactions on , Volume: 39 , Issue: 6 , Nov.-Dec.
2003
Pages:1614 - 1621

[Abstract] [PDF Full-Text (815 KB)] **IEEE JNL**

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4 **Lensed plastic optical fiber employing concave end filled with high-inc resin**
Sakata, H.; Imada, A.;

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Lightwave Technology, Journal of , Volume: 20 , Issue: 4 , April 2002
Pages:638 - 642

[Abstract]   [PDF Full-Text (310 KB)]   IEEE JNL

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5 **Measurements of solder bump lifetime as a function of underfill mater properties**
Nysaether, J.B.; Lundstrom, P.; Liu, J.;
Components, Packaging, and Manufacturing Technology, Part A, IEEE Transactic
on [see also Components, Hybrids, and Manufacturing Technology, IEEE
Transactions on] , Volume: 21 , Issue: 2 , June 1998
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6 **Explosion model applied to an intense pulsed plasma source for thin fi deposition**
Pedrow, P.D.; Goyal, K.O.; Mabalingham, R.; Osman, M.A.;
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[Abstract]   [PDF Full-Text (216 KB)]   IEEE JNL

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7 **Compliant bumps for adhesive flip-chip assembly**
Keswick, K.; German, R.L.; Breen, M.; Nolan, R.;
Components, Packaging, and Manufacturing Technology, Part B: Advanced
Packaging, IEEE Transactions on [see also Components, Hybrids, and
Manufacturing Technology, IEEE Transactions on] , Volume: 18 , Issue: 3 , Aug
1995
Pages:503 - 510

[Abstract]   [PDF Full-Text (752 KB)]   IEEE JNL

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8 **Polymeric cable terminators under accelerated aging in a fog chambei**
Gorur, R.S.; Cherney, E.A.; Hackam, R.;
Power Delivery, IEEE Transactions on , Volume: 4 , Issue: 2 , April 1989
Pages:842 - 849

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9 **Effective indexing and filtering for similarity search in large biosequei databases**
Ozturk, O.; Ferhatosmanoglu, H.;
Bioinformatics and Bioengineering, 2003. Proceedings. Third IEEE Symposium c
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Pages:359 - 366

[Abstract]   [PDF Full-Text (844 KB)]   IEEE CNF

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10 **Augmenting SSEs with structural properties for rapid protein structu comparison**
Chern-Hooi Chionh; Zhiyong Huang; Kian-Lee Tan; Zhen Yao;
Bioinformatics and Bioengineering, 2003. Proceedings. Third IEEE Symposium c
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Pages:341 - 348

[Abstract]   [PDF Full-Text (401 KB)]   **IEEE CNF**

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11 Nodal distance algorithm: calculating a phylogenetic tree comparison metric
Bluis, J.; Shin, D.G.;
Bioinformatics and Bioengineering, 2003. Proceedings. Third IEEE Symposium c
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Pages:87 - 94

[Abstract]   [PDF Full-Text (333 KB)]   **IEEE CNF**

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12 Estimation of the platelet glycoprotein (GP) Ib - von Willebrand factc (vWf) bond lifetime under hydrodynamic flow
Anand Kumar, R.; Jing-fei Dong; Lopez, J.A.; Cruz, M.A.; McIntire, L.V.;
[Engineering in Medicine and Biology, 2002. 24th Annual Conference and the Annual Fall Meeting of the Biomedical Engineering Society] EMBS/BMES Conference, 2002. Proceedings of the Second Joint , Volume: 1 , 2002
Pages:347 - 348 vol.1

[Abstract]   [PDF Full-Text (238 KB)]   **IEEE CNF**

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13 Thermochromic behavior in novel conducting polymers at the solid-liquid phase transition
Onoda, M.; Tada, K.;
Dielectric Liquids, 2002. ICDL 2002. Proceedings of 2002 IEEE 14th Internation:
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Pages:373 - 376

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14 A study of image retrieval by anchoring
Natsev, A.; Smith, J.R.;
Multimedia and Expo, 2002. ICME '02. Proceedings. 2002 IEEE International Conference on , Volume: 2 , 26-29 Aug. 2002
Pages:421 - 424 vol.2

[Abstract]   [PDF Full-Text (542 KB)]   **IEEE CNF**

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15 A novel method of measuring the thickness of hydrated ultrathin polymer film by the force curve of atomic force microscopy
Wu, C.C.; Chang, H.C.;
Microtechnologies in Medicine & Biology 2nd Annual International IEEE-EMB Special Topic Conference on , 2-4 May 2002
Pages:27 - 30

[Abstract]   [PDF Full-Text (436 KB)]   **IEEE CNF**

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16 **Bio-functionalized neurochips**
Tiefenauer, L.X.; Sorribas, H.; Padeste, C.; Stricker, C.;
Engineering in Medicine and Biology Society, 2001. Proceedings of the 23rd Anr
International Conference of the IEEE , Volume: 1 , 25-28 Oct. 2001
Pages:733 - 736 vol.1

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17 **Effect of intermolecular interactions on charge transport and light-emission in organic light emitting diodes**
Lupton, J.M.; Samuel, I.D.W.; Beavington, R.; Burn, P.L.; Bassler, H.;
Lasers and Electro-Optics Europe, 2000. Conference Digest. 2000 Conference oı
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18 **Computer biochemistry and molecular technology of the underwater biosensor creation: study of the natural chemical substance population**
Zamyatnin, A.A.;
Underwater Technology, 2000. UT 00. Proceedings of the 2000 International
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Pages:451 - 456

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19 **A new linguistic fuzzy approach to recognition of olfactory signals**
Lazzerini, B.; Maggiore, A.; Marcelloni, F.;
Neural Networks, 1999. IJCNN '99. International Joint Conference on , Volume:
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Pages:3225 - 3229 vol.5

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20 **Fractals for hybrid orbitals in protein models**
Torrens, F.; Sanchez-Marin, J.; Nebot-Gil, I.;
Information Technology Applications in Biomedicine, 1998. ITAB 98. Proceeding
1998 IEEE International Conference on , 16-17 May 1998
Pages:45 - 50

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21 **Experimental and numerical study of underfill encapsulation of flip-chips using conductive epoxy polymer bumps**
Ni, G.; Gordon, M.H.; Schmidt, W.F.; Muyshondt, A.;
Electronic Components and Technology Conference, 1997. Proceedings., 47th
, 18-21 May 1997
Pages:859 - 865

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22 **Basic investigations of the performance of droplets on electrically stressed polymer surfaces**
Kloes, H.-J.; Koenig, D.;
Electrical Insulation and Dielectric Phenomena, 1997. IEEE 1997 Annual Report.
Conference on , Volume: 2 , 19-22 Oct. 1997
Pages:374 - 377 vol.2

[Abstract]   [PDF Full-Text (504 KB)]   **IEEE CNF**

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23 **New hashing techniques and their application to a protein structure database system**
Akutsu, T.; Onizuka, K.; Ishikawa, M.;
System Sciences, 1995. Vol. V. Proceedings of the Twenty-Eighth Hawaii
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Pages:197 - 206 vol.5

[Abstract]   [PDF Full-Text (640 KB)]   **IEEE CNF**

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24 **Breakdown voltages of dielectric-coated sphere-plane electrode configurations in high vacuum**
Konig, D.; Heinemeyer, R.; Scherb, V.;
Electrical Insulation, 1988., Conference Record of the 1988 IEEE International
Symposium on , 5-8 June 1988
Pages:60 - 63

[Abstract]   [PDF Full-Text (292 KB)]   **IEEE CNF**

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1 Fast detection of common geometric substructure in proteins
L. Paul Chew, Dan Huttenlocher, Klara Kedem, Jon Kleinberg
April 1999 Proceedings of the third annual international conference on Computationa

Full text available: 📄 pdf(1.18 MB)   Additional Information: full citation, references, index terms

2 Detection of three-dimensional patterns of atoms in chemical structures
Arthur M. Lesk
April 1979   Communications of the ACM, Volume 22 Issue 4

Full text available: 📄 pdf(599.69 KB)   Additional Information: full citation, abstract, refer

An algorithm for detecting occurrences of a three-dimensional pattern of objects
The search technique presented uses the geometric structure of the pattern to c
candidates for matching. This is useful in cases where the properties of each atc
adequately limit the number of sets of possible matchings. Several applications
are: (1) i ...

Keywords: chemical structure search, crystal-structure analysis, drug analysis a
three-dimensional pattern recognition

3 Hybrid genetic algorithms for polypeptide energy minimization
Laurence D. Merkle, Robert L. Gaulke, Gary B. Lamont, George H. Gates, Ruth Pac
February 1996   Proceedings of the 1996 ACM symposium on Applied Computir

Full text available: pdf(689.75 KB)   Additional Information: full citation, references, citing

Keywords: Baldwinian evolution, conjugate gradient, genetic algorithms, probab folding

4 Keynote address: Visualization challenges for a new cyberpharmaceutical (
Russell J. Turner, Kabir Chaturvedi, Nathan J. Edwards, Daniel Fasulo, Aaron L. Ha
Jason R. Miller, Knut Reinert, Karin A. Remington, Russell Schwartz, Brian Walenz,
October 2001   Proceedings of the IEEE 2001 symposium on parallel and large-data

Full text available: pdf(3.07 MB)   Additional Information: full citation, abstract, reference

In recent years, an explosion in data has been profoundly changing the field of l
areas of expertise, particularly in the handling of data. One vital area that has s
to communicate the large quantities of diverse and complex information that is l
a number of visualization problems in the course of developing tools for bioinfor
data generation ...

5 Polypeptide structure prediction: real-value versus binary hybrid genetic alc
Charles E. Kaiser, Gary B. Lamont, Laurence D. Merkle, George H. Gates, Ruth Pac
April 1997   Proceedings of the 1997 ACM symposium on Applied computing

Full text available: pdf(727.53 KB)   Additional Information: full citation, references, citing

Keywords: genetic algorithms, hybrid genetic algorithms, polypeptide structure genetic algorithms

6 The threading approach to the inverse protein folding problem
Temple F. Smith, Loredana Lo Conte, Jadwiga Bienkowska, Bob Rogers, Chrysanth
January 1997   Proceedings of the first annual international conference on Computati

Full text available: pdf(680.95 KB)   Additional Information: full citation, references, citings, in(

7 Coupled optimization in protein docking

Julie C. Mitchell, J. Ben Rosen, Andrew T. Phillips, Lynn F. Ten Eyck

April 1999 Proceedings of the third annual international conference on Computationa

Full text available: pdf(702.99 KB)   Additional Information: full citation, references, index term

8 Interactive computer graphics and macromolecular structures

Peter J. Bond

March 1972 ACM SIGGRAPH Computer Graphics , Proceedings of the 1972 SIGGRAF medicine, Volume 6 Issue 4

Full text available: pdf(935.08 KB)   Additional Information: full citation, abstract, referen

In 1964 on Project MAC at MIT, Levinthal and Langridge first applied interactive building (1, 2). Since then a number of laboratories have developed computer g needs (3, 4, 5, 6). I shall begin by describing the system that we have develope Graphics Laboratory during the past year to investigate macromolecular structui

9 Minimizing the Lennard-Jones potential function on a massively parallel cor

G. L. Xue, R. S. Maier, J. B. Rosen

August 1992   Proceedings of the 6th international conference on Supercomputii

Full text available: pdf(636.32 KB)   Additional Information: full citation, abstract, references, c

The Lennard-Jones potential energy function arises in the study of low-energy s' cluster statics. This paper presents a mathematical treatment of the potential fu function of the cluster size, in both two and three dimensional configurations. Th minimization of a linear chain, or polymer, in two-dimensional space to illustrate cluster size. An algorithm is ...

10 Large scale molecular dynamics simulations with fast multipole implementa

Zhiqiang Wang, James A. Lupo, Alan M. McKenney, Ruth Pachter

January 1999 Proceedings of the 1999 ACM/IEEE conference on Supercomputing (CL

Full text available: pdf(748.81 KB)   Additional Information: full citation, references, citings, index terms

11 Simulation and preferences: Virtual spring manipulators for particle steerinç responsive workbench

Michal Koutek, Jeroen van Hees, Frits H. Post, A. F. Bakker

May 2002   Proceedings of the workshop on Virtual environments 2002

Full text available: pdf(6.52 MB)   Additional Information: full citation, abstract, referenc

In this paper we present new virtual spring manipulator-based tools for steering simulations in virtual environments. We briefly overview the MolDRIVE system, steering environment for molecular dynamics real-time simulations, which is the implementation.Our study concentrates on visual feedback tools. We compare a with two other methods using a spring mani ...

12 Approximation of protein structure for fast similarity measures

Fabian Schwarzer, Itay Lotan

April 2003 Proceedings of the seventh annual international conference on Comput;

Full text available: pdf(212.43 KB)   Additional Information: full citation, abstract, referen

It is shown that structural similarity between proteins can be decided well with r
common similarity measures. The full C? representation contains redundant info
topology of proteins and a limit on their compactness due to excluded volume. /
proteins justifies approximating subchains by their centers of mass. For not too
and ...

Keywords: approximation of structure, nearest-neighbor search, protein structu

13 SIGSAM BULLETIN: Computer algebra in the life sciences

Michael P. Barnett

December 2002   ACM SIGSAM Bulletin, Volume 36 Issue 4

Full text available: pdf(240.15 KB)   Additional Information: full citation, abstract,

This note (1) provides references to recent work that applies computer algebra ·
literature that explains the biological background of each application, (3) states
(4) mentions the benefits of CA, and (5) suggests some topics for future work.

14 Extracting structural information using time-frequency analysis of protein NI

Christopher James Langmead, Bruce Randall Donald

April 2001 Proceedings of the fifth annual international conference on Computati·

Full text available: pdf(623.73 KB)   Additional Information: full citation, abstract, referen·

High-throughput, data-directed computational protocols for *Stru*
are required in order to evaluate the protein products of genes f
comparable to current gene-sequencing technology. To develop
are required that can quickly extract significantly more structur;
experimental data. This paper presents a new class of signal prc
magnetic re ...

[15] GRAMPS - A graphics language interpreter for real-time, interactive, three-animation

T. J. O'Donnell, Arthur J. Olson

August 1981 ACM SIGGRAPH Computer Graphics , Proceedings of the 8th annual con interactive techniques, Volume 15 Issue 3

Full text available: pdf(1.19 MB)   Additional Information: full citation, abstract, references, c

GRAMPS, a graphics language interpreter has been developed in FORTRAN 77 to interactive vector display list processor (Evans and Sutherland Multi-Picture-Sys language make it very useful and convenient for real-time scene construction, n language syntax allows natural interaction with scene elements as well as easy, devices. GRAMPS facilitates the ...

Keywords: Graphics language interpreter, Picture editor, Real-time animation, V

[16] Molecular simulation of rheological properties using massively parallel supe

R. K. Bhupathiraju, S. T. Cui, S. Gupta, H. D. Cochran, P. T. Cummings

November 1996   Proceedings of the 1996 ACM/IEEE conference on Supercomput

Full text available: pdf(120.44 KB)   Additional Information: full citation, abstract, referenc

Advances in parallel supercomputing now make possible molecular-based engine soon revolutionize many technologies, such as those involving polymers and the have developed a suite of message-passing codes for classical molecular simula amorphous materials and have completed a number of demonstration calculatio technological importance with each (describe ...

[17] Using motion planning to map protein folding landscapes and analyze foldin

Nancy M. Amato, Ken A. Dill, Guang Song

April 2002   Proceedings of the sixth annual international conference on Computat

Full text available: pdf(4.00 MB)   Additional Information: full citation, abstract, references, c

We present a novel approach for studying the kinetics of protein folding. The fra planning techniques called *probabilistic roadmap* methods (prms) that have bee success. In our previous work, we used a Prm-based technique to study protein and obtained encouraging results. In this paper, we describe how our motion pla protein foldin ...

18 Protein structure determination using protein threading and sparse NMR dɛ

Ying Xu, Dong Xu, Oakley H. Crawford, J. Ralph Einstein, Engin Serpersu

April 2000   Proceedings of the fourth annual international conference on Computati

Full text available: pdf(663.42 KB)   Additional Information: full citation, abstract, refere

It is well known that the NMR method for protein structure detei proteins and that its effectiveness decreases very rapidly as the beyond about 30 kD. We have recently developed a method for that can fully utilize partial NMR data as calculation constraints. threading algorithm that guarantees to find a globally optimal ai sequence and a template structure, ...

Keywords: NMR, energy minimization, fold recognition, protein ɛ threading

19 Architectural requirements of parallel scientific applications with explicit cor

R. Cypher, A. Ho, S. Konstantinidou, P. Messina

May 1993 ACM SIGARCH Computer Architecture News , Proceedings of the 20th anr Computer architecture, Volume 21 Issue 2

Full text available: pdf(1.29 MB)   Additional Information: full citation, abstract, references, c

This paper studies the behavior of scientific applications running on distributed r quantify the floating point, memory, I/O and communication requirements of hi(perform explicit communication. In addition to quantifying these requirements fi processors, we develop analytical models for the effects of changing the problen several of the ...

20 Assessment of ab initio protein structure prediction

Arthur M. Lesk

March 1998 Proceedings of the second annual international conference on Computat

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21 De Novo peptide sequencing via tandem mass spectrometry: a graph-theol
Vlado Dan?ík, Theresa A. Addona, Karl R. Clauser, James E. Vath
April 1999 Proceedings of the third annual international conference on Computationa
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22 Regression analysis of multiple protein structures
Thomas D. Wu, Trevor Hastie, Scott C. Schmidler, Douglas L. Brutlag
March 1998 Proceedings of the second annual international conference on Computat
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23 Finding the consensus shape for a protein family
L. Paul Chew, Klara Kedem
June 2002   Proceedings of the eighteenth annual symposium on Computational (
Full text available: pdf(211.67 KB)   Additional Information: full citation, abstract, referen

We define and prove properties of the *consensus shape for a family of proteins*, compact summary of the significant structural information for a protein family. I geometric relationship between corresponding alpha carbons then that relations In particular, distances and angles that are consistent across family members ar the spacin ...

Keywords: dynamic programming, multiple alignment, protein alignment, protei RMS

24 The NOESY jigsaw: automated protein secondary structure and main-chair NMR data
Chris Bailey-Kellogg, Alik Widge, John J. Kelley, Marcelo J. Berardi, John H. Bushwi
April 2000   Proceedings of the fourth annual international conference on Computati
Full text available: pdf(907.80 KB)   Additional Information: full citation, abstract, refe

High-throughput, data-directed computational protocols for *Stru* are required in order to evaluate the protein products of genes f comparable to current gene-sequencing technology. This paper novel high-throughput, automated approach to protein structure magnetic resonance (NMR). JIGSAW applies graph algorithms ai techniques, enf ...

25 The hierarchical organization of molecular structure computations
Cheng Che Chen, Jaswinder Pal Singh, Russ B. Altman
March 1998   Proceedings of the second annual international conference on Computat
Full text available: pdf(992.98 KB)   Additional Information: full citation, references, index ter

26 Algorithmic determination of core positions in the VL and VH domains of im
Israel Gelfand, Alexander Kister, Casimir Kulikowski, Ognyan Stoyanov
March 1998   Proceedings of the second annual international conference on Computa
Full text available: pdf(962.19 KB)   Additional Information: full citation, references, index i

27 Trilogy: discovery of sequence-structure patterns across diverse proteins

Phil Bradley, Peter S. Kim, Bonnie Berger

April 2002   Proceedings of the sixth annual international conference on Computati

Full text available: 📄 pdf(3.86 MB)   Additional Information: full citation, abstract, references

We describe a new computer program, Trilogy, for the automated discovery of s
Trilogy implements a pattern discovery algorithm that begins with an exhaustive
patterns; a subset of these patterns are selected as seeds for an extension proc
identified. A key feature of the method is explicit treatment of both the sequenc
motifs: each Trilogy pattern is a pair ...

28 Massively parallel simulations of diffusion in dense polymeric structures

Jean-Loup Faulon, J. David Hobbs, David M. Ford, Robert T. Wilcox

November 1997   Proceedings of the 1997 ACM/IEEE conference on Supercomput

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An original computational technique to generate close-to-equilibrium dense poly
small gases are studied on the equilibrated structures using massively parallel n
the Intel Teraflops (9216 Pentium Pro processors) and Intel Paragon (1840 proc
state-of-the-art equilibration methods this new technique appears to be faster b
advantage of the technique i ...

Keywords: gas diffusion, molecular builder, molecular dynamics, polymer, terafl

29 Determining contact energy function for continuous state models of globula

Y. Zenmei Ohkubo, Gordon M. Crippen

April 2000   Proceedings of the fourth annual international conference on Computati

Full text available: 📄 pdf(698.70 KB)   Additional Information: full citation, abstract,

One of the approaches to protein structure prediction is to obtai
recognize the native conformation of a given sequence among a
discriminations can be done by assigning the lowest energy to tl
guarantee that the native is in the zoo. Well-adjusted functions,
for other (near-) natives. Here the aim is the discrimination at r
difference between the ...

30 A solvation potential with improved contact definitions and optimized by ext

Alan A. Dombkowski, Gordon M. Crippen

April 1999   Proceedings of the third annual international conference on Computation

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31 A framework for improving protein structure predictions by teamwork
Luigi Palopoli, Giorgio Terracina
January 2003   Proceedings of the First Asia-Pacific bioinformatics conference on Bioi
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Pridicting the three dimensional structure of proteins is a difficult task. In the la:
proposed for performing this task taking into account different protein chemical
growing number of protein structure prediction tools is becoming available, som
either some aspects of the predictions or on some categories of proteins. In this
apply different pr ...

Keywords: collaborative computation, hetrogeneous representations, multi-ager

32 Session 19: biomedical applications: Parallel protein structure determinatio
Cheng Che Chen, Jaswinder Pal Singh, William B. Poland, Russ B. Altman
November 1994   Proceedings of the 1994 ACM/IEEE conference on Supercomp
Full text available: 🔲 pdf(957.79 KB)   Additional Information: full citation, abstract, r

Molecular structure determination is an important task in biology because of the
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33 An algorithm with linear complexity for interactive, physically-based modelir
Mark C. Surles
July 1992 ACM SIGGRAPH Computer Graphics , Proceedings of the 19th annual conf
interactive techniques, Volume 26 Issue 2
Full text available: 🔲 pdf(1.76 MB)   Additional Information: full citation, references, citing:

Keywords: Lagrange multiplier method, constrain systems, molecular modeling

34 The principled design of large-scale recursive neural network architectures
prediction problem
Pierre Baldi, Gianluca Pollastri
December 2003   The Journal of Machine Learning Research, Volume 4
Full text available: 🔲 pdf(231.40 KB)   Additional Information: full citation

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(DAGs) to connect visible and hidden node variables; (2) parameterization of th
its parent variables by feedforward neural networks; and (3) application of weig
DAG connections to capture s ...

35 A dimensionality reduction approach to modeling protein flexibility

Miguel L. Teodoro, George N. Phillips, Lydia E. Kavraki

April 2002   Proceedings of the sixth annual international conference on Computat

Full text available: pdf(2.03 MB)   Additional Information: full citation, abstract, reference

Proteins are involved either directly or indirectly in all biological processes in livi
that conformational changes of proteins can critically affect their ability to bind (
modeling protein motion and flexibility will contribute to the understanding of ke
protein flexibility has proven a very difficult task. Experimental laboratory meth(
...

36 Parallel hierarchical molecular structure estimation

Cheng Che Chen, Jaswinder Pal Singh, Russ B. Altman

November 1996   Proceedings of the 1996 ACM/IEEE conference on Supercomput

Full text available: pdf(220.93 KB)   Additional Information: full citation, abstract, references, (

Determining the structure of biological macromolecules such as proteins and nu(
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37 New contact measures for the protein docking problem

Hans-Peter Lenhof

January 1997 Proceedings of the first annual international conference on Computatic

Full text available: pdf(1.30 MB)   Additional Information: full citation, references, citings, index te

38 Multiple molecular dynamics simulations of a 28mer oligopeptide reveal enl space

Sangeeta Sawant, A. S. Kolaskar

January 2003   Proceedings of the First Asia-Pacific bioinformatics conference on Bio:

Full text available: pdf(1.53 MB)   Additional Information: full citation, abstract, reference

A strategy using multiple runs of MD simulations has been used for conformatioi
demonstrate the effectiveness of the strategy to sample the conformational spa(
MD simulation. Further, the use of cluster analysis and C? distances has been m
peptide that are generated in the relatively short time scale simulations.

Keywords: cluster analysis, conformational searches, multiple MD simulations, o

[39] A unified sequence-structure classification of protein sequences: combining the protein space

Golan Yona, Michael Levitt

April 2000   Proceedings of the fourth annual international conference on Computati

Full text available: pdf(952.18 KB)   Additional Information: full citation, abstract

> We analyze all known protein sequences in search for a global m
> consistent in terms of both sequence and structure. Our goal is t
> protein domains, beyond those detected by sequence-based me
> three-dimensional (3D) model for each of the sequences that ar
> known 3D structure. This analysis uses both sequence and struc
> of all protein sequences in a ...

[40] Structural alignment of large—size proteins via lagrangian relaxation

Alberto Caprara, Giuseppe Lancia

April 2002   Proceedings of the sixth annual international conference on Computat

Full text available: pdf(1.65 MB)   Additional Information: full citation, abstract, reference

> We illustrate a new approach to the Contact Map Overlap problem for the compa
> is based on formulating the problem as an integer linear program and then rela
> constraints. This relaxation is solved by computing a sequence of simple alignm
> near--optimal Lagrangian multipliers are found by subgradient optimization. By
> speedup over the best ...

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21 De Novo peptide sequencing via tandem mass spectrometry: a graph-theo
Vlado Dan?ík, Theresa A. Addona, Karl R. Clauser, James E. Vath
April 1999 Proceedings of the third annual international conference on Computation;
Full text available: pdf(1.24 MB)   Additional Information: full citation, references, citings, index ter

22 Regression analysis of multiple protein structures
Thomas D. Wu, Trevor Hastie, Scott C. Schmidler, Douglas L. Brutlag
March 1998 Proceedings of the second annual international conference on Computat
Full text available: pdf(1.04 MB)   Additional Information: full citation, references, index term

23 Finding the consensus shape for a protein family
L. Paul Chew, Klara Kedem
June 2002   Proceedings of the eighteenth annual symposium on Computational (

Full text available: 🔁 pdf(211.67 KB)   Additional Information: full citation, abstract, referen

We define and prove properties of the *consensus shape for a family of proteins*, compact summary of the significant structural information for a protein family. I geometric relationship between corresponding alpha carbons then that relations In particular, distances and angles that are consistent across family members an the spacin ...

Keywords: dynamic programming, multiple alignment, protein alignment, protei RMS

24 The NOESY jigsaw: automated protein secondary structure and main-chair NMR data
Chris Bailey-Kellogg, Alik Widge, John J. Kelley, Marcelo J. Berardi, John H. Bushw
April 2000   Proceedings of the fourth annual international conference on Computati

Full text available: 🔁 pdf(907.80 KB)   Additional Information: full citation, abstract, refe

High-throughput, data-directed computational protocols for *Stru* are required in order to evaluate the protein products of genes f comparable to current gene-sequencing technology. This paper novel high-throughput, automated approach to protein structure magnetic resonance (NMR). JIGSAW applies graph algorithms an techniques, enf ...

25 The hierarchical organization of molecular structure computations
Cheng Che Chen, Jaswinder Pal Singh, Russ B. Altman
March 1998 Proceedings of the second annual international conference on Computat

Full text available: 🔁 pdf(992.98 KB)   Additional Information: full citation, references, index ter

26 Algorithmic determination of core positions in the VL and VH domains of im
Israel Gelfand, Alexander Kister, Casimir Kulikowski, Ognyan Stoyanov
March 1998 Proceedings of the second annual international conference on Computa

Full text available: 🔁 pdf(962.19 KB)   Additional Information: full citation, references, index 1

27 Trilogy: discovery of sequence-structure patterns across diverse proteins

Phil Bradley, Peter S. Kim, Bonnie Berger

April 2002   Proceedings of the sixth annual international conference on Computati

Full text available: 🗒 pdf(3.86 MB)   Additional Information: full citation, abstract, references

> We describe a new computer program, Trilogy, for the automated discovery of s
> Trilogy implements a pattern discovery algorithm that begins with an exhaustive
> patterns; a subset of these patterns are selected as seeds for an extension proc
> identified. A key feature of the method is explicit treatment of both the sequenc
> motifs: each Trilogy pattern is a pair ...

28 Massively parallel simulations of diffusion in dense polymeric structures

Jean-Loup Faulon, J. David Hobbs, David M. Ford, Robert T. Wilcox

November 1997   Proceedings of the 1997 ACM/IEEE conference on Supercompul

Full text available: 🗒 pdf(92.74 KB)   Additional Information: full citation, abstract,

> An original computational technique to generate close-to-equilibrium dense poly
> small gases are studied on the equilibrated structures using massively parallel n
> the Intel Teraflops (9216 Pentium Pro processors) and Intel Paragon (1840 proc
> state-of-the-art equilibration methods this new technique appears to be faster b
> advantage of the technique i ...
>
> Keywords: gas diffusion, molecular builder, molecular dynamics, polymer, terafl

29 Determining contact energy function for continuous state models of globula

Y. Zenmei Ohkubo, Gordon M. Crippen

April 2000   Proceedings of the fourth annual international conference on Computati

Full text available: 🗒 pdf(698.70 KB)   Additional Information: full citation, abstract,

> One of the approaches to protein structure prediction is to obtai
> recognize the native conformation of a given sequence among a
> discriminations can be done by assigning the lowest energy to th
> guarantee that the native is in the zoo. Well-adjusted functions,
> for other (near-) natives. Here the aim is the discrimination at r
> difference between the ...

30 A solvation potential with improved contact definitions and optimized by ext

Alan A. Dombkowski, Gordon M. Crippen

April 1999 Proceedings of the third annual international conference on Computationa

Full text available: 🗒 pdf(1.02 MB)   Additional Information: full citation, references, index terms

31 A framework for improving protein structure predictions by teamwork
Luigi Palopoli, Giorgio Terracina
January 2003   Proceedings of the First Asia-Pacific bioinformatics conference on Bioi

Full text available: 📄 pdf(306.78 KB)   Additional Information: full citation, abstract, referenc

Pridicting the three dimensional structure of proteins is a difficult task. In the las proposed for performing this task taking into account different protein chemical growing number of protein structure prediction tools is becoming available, som either some aspects of the predictions or on some categories of proteins. In this apply different pr ...

Keywords: collaborative computation, hetrogeneous representations, multi-ager

32 Session 19: biomedical applications: Parallel protein structure determinatio
Cheng Che Chen, Jaswinder Pal Singh, William B. Poland, Russ B. Altman
November 1994   Proceedings of the 1994 ACM/IEEE conference on Supercomp

Full text available: 📄 pdf(957.79 KB)   Additional Information: full citation, abstract, r

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33 An algorithm with linear complexity for interactive, physically-based modelir
Mark C. Surles
July 1992 ACM SIGGRAPH Computer Graphics , Proceedings of the 19th annual conf interactive techniques, Volume 26 Issue 2

Full text available: 📄 pdf(1.76 MB)   Additional Information: full citation, references, citing:

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34 The principled design of large-scale recursive neural network architectures prediction problem
Pierre Baldi, Gianluca Pollastri
December 2003   The Journal of Machine Learning Research, Volume 4

Full text available: 📄 pdf(231.40 KB)   Additional Information: full citation

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April 2002   Proceedings of the sixth annual international conference on Computat

Full text available: ⊠ pdf(2.03 MB)   Additional Information: full citation, abstract, reference

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...

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November 1996   Proceedings of the 1996 ACM/IEEE conference on Supercomput

Full text available: ⊠ pdf(220.93 KB)   Additional Information: full citation, abstract, references, c

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37 New contact measures for the protein docking problem

Hans-Peter Lenhof

January 1997 Proceedings of the first annual international conference on Computatic

Full text available: ⊠ pdf(1.30 MB)   Additional Information: full citation, references, citings, index te

38 Multiple molecular dynamics simulations of a 28mer oligopeptide reveal enl
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Sangeeta Sawant, A. S. Kolaskar

January 2003   Proceedings of the First Asia-Pacific bioinformatics conference on Bioi

Full text available: ⊠ pdf(1.53 MB)   Additional Information: full citation, abstract, reference

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MD simulation. Further, the use of cluster analysis and C? distances has been m
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39 A unified sequence-structure classification of protein sequences: combining the protein space

Golan Yona, Michael Levitt

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Full text available: pdf(952.18 KB)   Additional Information: full citation, abstract

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40 Structural alignment of large—size proteins via lagrangian relaxation

Alberto Caprara, Giuseppe Lancia

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Full text available: pdf(1.65 MB)   Additional Information: full citation, abstract, reference

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41 Accurate performance evaluation, modelling and prediction of a message p middleware
Michela Taufer, Thomas Stricker
November 1998   Proceedings of the 1998 ACM/IEEE conference on Supercompul
Full text available: 🖻 html(85.30 KB)   Additional Information: full citation, abstract, refe

> In distributed and vectorized computing there is a large number of highly differe
> application could run on. Therefore most traditional parallel codes are ill equippe
> usage or their behavior at run time and the corresponding data are rarely publis
> of an application and its platform systematically. As an improvement over the cu
> integrated approach to pe ...
>
> Keywords: PVM, application design methods, computer architecture, molecular (
> middleware, performance monitoring, scientific application codes

42 Chain growth algorithms for HP-type lattice proteins
Erich Bornberg-Bauer
January 1997 Proceedings of the first annual international conference on Computatic
Full text available: 🗋 pdf(1.13 MB)   Additional Information: full citation, references, citings, index 1

> Keywords: chain growth algorithm, cotranslational foldability, lattice models, loc

43 Interactive modeling enhanced with constraints and physics with applicatio

Mark C. Surles

June 1992   Proceedings of the 1992 symposium on Interactive 3D graphics

Full text available: pdf(1.03 MB)   Additional Information: full citation, references, citings, inde›

44 Comprehensive statistical method for protein fold recognition

Jadwiga R. Bie?kowska, Lihua Yu, Sophia Zarakhovich, Robert G. Rogers, Temple I

April 2000   Proceedings of the fourth annual international conference on Computati

Full text available: pdf(1.08 MB)   Additional Information: full citation, abstract, r‹

> We present a protein fold recognition method that uses a compr
> of structural Hidden Markov Models (HMMs). The structure/fold ı
> the probabilities of all sequence-to-structure alignments Conven
> dictate that the optimal alignment can give an estimate of the lc
> conformation imposed by the structural model. The alignment is
> that is interpret ...

45 Multi Relational Data Mining (MRDM): Multi-relational data mining: an intro‹

Sašo Džeroski

July 2003   ACM SIGKDD Explorations Newsletter, Volume 5 Issue 1

Full text available: pdf(1.71 MB)   Additional Information: full citation, abstract, refere‹

> Data mining algorithms look for patterns in data. While most existing data minir
> data table, multi-relational data mining (MRDM) approaches look for patterns th
> a relational database. In recent years, the most common types of patterns and ‹
> have been extended to the multi-relational case and MRDM now encompasses ṉ
> discovery, MR decision tree ...
>
> Keywords: inductive logic programming, multi-relational data mining, relational
> relational decision trees, relational distance-based methods

46 RAPID: randomized pharmacophore identification for drug design

P. W. Finn, L. E. Kavraki, J.-C. Latombe, R. Motwani, C. Shelton, S. Venkatasubrar

August 1997   Proceedings of the thirteenth annual symposium on Computational ge·

Full text available: pdf(1.28 MB)   Additional Information: full citation, references, citings, index term‹

47 A new method for modeling and solving the protein fold recognition problen
Ying Xu, Dong Xu, Edward C. Uberbacher
March 1998 Proceedings of the second annual international conference on Computat

Full text available: 📄 pdf(893.53 KB)   Additional Information: full citation, references, citings, inde>

48 ARIADNE: pattern-directed inference and hierarchical abstraction in proteir
Richard H. Lathrop, Teresa A. Webster, Temple F. Smith
November 1987   Communications of the ACM, Volume 30 Issue 11

Full text available: 📄 pdf(1.30 MB)   Additional Information: full citation, abstract, references, citing:

The macro-molecular structural conformations of proteins exhibit higher order r(
complicated by many factors. ARIADNE searches for similarities between structu
structure at levels more abstract than the primary sequence.

49 Computational approach to the statistical mechanics of protein folding
Ming-Hong Hao, Harold A. Scheraga
December 1995 Proceedings of the 1995 ACM/IEEE conference on Supercomputing (

Full text available: 📄 pdf(5.92 MB) 📄 html(2.06 KB)   Additional Information: full citation, references, index

50 A complete and effective move set for simplified protein folding
Neal Lesh, Michael Mitzenmacher, Sue Whitesides
April 2003   Proceedings of the seventh annual international conference on Compute

Full text available: 📄 pdf(521.61 KB)   Additional Information: full citation, abstract, referenc

We present new lowest energy configurations for several large benchmark probl
hydrophobic-hydrophilic model. We found these solutions with a generic implem
apparently novel set of transformations that we call *pull moves*. Our experiment
best solutions in 3 to 14 hours, on average. Pull moves appear quite effective ar
search algorithms for the problem. Addit ...

Keywords: local moves, protein folding, tabu search

51 Session P8: nature visualization: Visualizing dynamic molecular conformati

Johannes Schmidt-Ehrenberg, Daniel Baum, Hans Christian Hege

October 2002   Proceedings of the conference on Visualization '02

Full text available: pdf(2.72 MB)   Additional Information: full citation, abstract, references,

The bioactivity of a molecule strongly depends on its metastable conformational these. Therefore, conformation analysis and visualization is a basic prerequisite processes.We present techniques for visual analysis of metastable molecular cor applicable methods for alignment of molecular geometries, as well as methods f metastable conformations. All an ...

Keywords: drug design, molecular conformation analysis, molecular modeling, u

52 Stochastic roadmap simulation: an efficient representation and algorithm fo

Mehmet Serkan Apaydin, Douglas L. Brutlag, Carlos Guestrin, David Hsu, Jean-Cla

April 2002   Proceedings of the sixth annual international conference on Computati

Full text available: pdf(2.03 MB)   Additional Information: full citation, abstract, references, cil

Classic techniques for simulating molecular motion, such as the Monte Carlo anc individual motion pathways one at a time and spend most of their time trying to energy landscape of a molecule. Their high computational cost prevents them fr pathways. We introduce Stochustic Roadmap Sirrrcllation (SRS), a new approac motion by simultaneously examining multip ...

53 Multi Relational Data Mining (MRDM): Biological applications of multi-relatic

David Page, Mark Craven

July 2003   ACM SIGKDD Explorations Newsletter, Volume 5 Issue 1

Full text available: pdf(1.12 MB)   Additional Information: full citation, abstract, referer

Biological databases contain a wide variety of data types, often with rich relatior multi-relational data mining techniques frequently are applied to biological data. of multi-relational data mining to biological data, taking care to cover a broad rz techniques.

54 Efficient database screening for rational drug design using pharmacophore

Steven M. LaValle, Paul W. Finn, Lydia E. Kavraki, Jeal-Claude Latombe

April 1999   Proceedings of the third annual international conference on Computatio

Full text available: pdf(1.70 MB)   Additional Information: full citation, references, citings,

55 On approximating arbitrary metrices by tree metrics

Yair Bartal

May 1998 Proceedings of the thirtieth annual ACM symposium on Theory of computi

Full text available: pdf(4.11 MB)   Additional Information: full citation, references, citings, index terms

56 Protein structure prediction by a data-level parallel algorithm

X. Zhang, D. Waltz, J. P. Mesirov

August 1989   Proceedings of the 1989 ACM/IEEE conference on Supercomputii

Full text available: pdf(907.03 KB)   Additional Information: full citation, abstract, referen

We have developed a software system, PHI-PSI, on the Connection Machine tha
use information from a database of 112 known protein structures (selected from
predict the structures of other proteins. The &phgr; and &psgr; angles of each a
forms with its immediate neighbors) in a protein are used to represent its 3-D st

57 Topology preserving dynamic load balancing for parallel molecular simulati

David F. Hegarty, M. T. Kechadi

November 1997   Proceedings of the 1997 ACM/IEEE conference on Supercomput

Full text available: pdf(227.39 KB)   Additional Information: full citation, abstract,

Understanding the behavior of molecular systems such as DNA and proteins is a
chemistry. Most research laboratories now have a collection of heterogeneous p
brought to bear on this problem - high end PCs, various different workstations, i
[8, 11, 20]. Much work is currently being done on programming tools to exploit
this work to date is aimed ...

58 Efficient algorithms for protein sequence design and the analysis of certain

Jon M. Kleinberg

April 1999   Proceedings of the third annual international conference on Computatioi

Full text available: pdf(1.52 MB)   Additional Information: full citation, references, citings, ir

59 Prediction of 3D structure of envelope glycoprotein of Sri Lanka strain of Ja

Urmila Kulkarni-Kale, A. S. Kolaskar

January 2003   Proceedings of the First Asia-Pacific bioinformatics conference on Bioi

Full text available: pdf(6.40 MB)   Additional Information: full citation, abstract, reference

This paper describes knowledge-based homology modeling studies of envelope (
Japanese encephalitis virus (JEVS). JEVS is a mosquito-borne *Flavivirus*, which i:
is a major structural antigen and is responsible for viral hemagglutination and n(
amino acids from the extra cellular domain of Egp of JEVS has been predicted u:
Tickborne enceph ...

Keywords: Japanese encephalitis virus, antigenic determinant, conformational e
modeling, loop modeling, molecular dynamics simulations, mutations, peptide v;
property, three-dimensional structure

60 Large a polynomial-time nuclear vector replacement algorithm for automate

Christopher James Langmead, Anthony Yan, Ryan Lilien, Lincong Wang, Bruce Rar

April 2003   Proceedings of the seventh annual international conference on Compute

Full text available: pdf(2.14 MB)   Additional Information: full citation, abstract, references

High-throughput NMR structural biology can play an important role in structural
procedure for high-throughput NMR resonance assignment for a protein of know
structure. These assignments are a prerequisite for probing protein-protein intei
dynamics by NMR. Assignments are also the starting point for structure determi
called *Nuclear Vector Replacement (NVR)* ...

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Best 200 shown

61 The side-chain positioning problem: a semidefinite programming formulatio
Bernard Chazelle, Carl Kingsford, Mona Singh
June 2003 Proceedings of the Paris C. Kanellakis memorial workshop on Principles o
Kanellakis memorial workshop on the occasion of his 50th birthday

Full text available: 📄 pdf(360.45 KB)   Additional Information: full citation, abstract, referen

Side-chain positioning is a central component of the protein structure prediction
large body of research. The problem is NP-complete; in fact, it is even inapproxi
variety of general search techniques and specialized heuristics. We investigate a
semidefinite program. We introduce two novel rounding schemes and provide th
effectiveness under various input ...

Keywords: protein side-chain positioning, randomized rounding, semidefinite pr(

62 Lab report special section: information retrieval research in the University o
Peter Willett
December 1997   ACM SIGIR Forum, Volume 31 Issue 2

Full text available: 📄 pdf(644.64 KB)   Additional Information: full citation, index terms

[63] The large scale parallelization of a conformational 3D Protein structure pre

Philip LoCascio, Kaizhi Yue, Peter Cummings, Ken Dill

November 1998   Proceedings of the 1998 ACM/IEEE conference on Supercomput

Full text available: html(20.65 KB)   Additional Information: full citation, abstract

We present here the design strategy and performance analysis of a large scale s
3D Protein structures. The unique challenges which will be investigated are the
clock run time through the parallelization process, and the production of an appl
massively parallel configuration (currently 1024 nodes of the Intel Paragon) reli
supercomput ...

Keywords: massively parallel algorithm, protein folding

[64] Efficient algorithms for local and global accessibility shading

Gavin Miller

July 1994   Proceedings of the 21st annual conference on Computer graphics and in

Full text available: pdf(1.11 MB) ps(13.03 MB)   Additional Information: full citation, abstract,

This paper discusses the use of two different approaches for computing the &ldc
These metrics characterize how easily a surface may be touched by a spherical
acceleration techniques for accessibility. The idea of surface accessibility is extei
accessibility” which measures the ability of a spherical probe to enter a s
locally on the surface. Th ...

Keywords: aging, surface accessibility shading, visualisation

[65] Molecular applications of volume rendering and 3-D texture maps

David S. Goodsell, Arthur J. Olson

May 1989   Proceedings of the 1989 Chapel Hill workshop on Volume visualization

Full text available: pdf(2.10 MB)   Additional Information: full citation, references, citings, index terms

Keywords: 3D texture map, ray-tracing, volume rendering

66 ## Spheres, molecules, and hidden surface removal

Dan Halperin, Mark H. Overmars

June 1994   Proceedings of the tenth annual symposium on Computational geom

Full text available: pdf(1.21 MB)   Additional Information: full citation, abstract, references, c

> We devise techniques to manipulate a collection of loosely interpenetrating sphe
> is motivated by the representation and manipulation of molecular configurations
> analyze the sphere model and point to its favorable properties that make it mor
> collection of spheres. For this special sphere model we present efficient algorithi
> for hidden su ...

67 ## Algorithmic issues in modeling motion

Pankaj K. Agarwal, Leonidas J. Guibas, Herbert Edelsbrunner, Jeff Erickson, Michae
Hershberger, Christian Jensen, Lydia Kavraki, Patrice Koehl, Ming Lin, Dinesh Man
David Mount, S. Muthukrishnan, Dinesh Pai, Elisha Sacks, Jack Snoeyink, Subhash

December 2002   ACM Computing Surveys (CSUR), Volume 34 Issue 4

Full text available: pdf(205.25 KB)   Additional Information: full citation, abstract, referen

> This article is a survey of research areas in which motion plays a pivotal role. Th
> approaches to modeling motion together with related data structures and algoril
> that lie ahead in producing a more unified theory of motion representation that '

> Keywords: Computational geometry, computer vision, mobile networks, modelir
> physical simulation, robotoics, spatio-temporal databases

68 ## Algorithmic strategies in combinatorial chemistry

Deborah Goldman, Sorin Istrail, Giuseppe Lancia, Antonio Piccolboni, Brian Walenz

February 2000 Proceedings of the eleventh annual ACM-SIAM symposium on Discrete

Full text available: pdf(940.84 KB)   Additional Information: full citation, references, index terms

69 ## Reconstructing a three-dimensional model with arbitrary errors

Bonnie Berger, Jon Kleinberg, Tom Leighton

March 1999   Journal of the ACM (JACM), Volume 46 Issue 2

Full text available: pdf(174.41 KB)   Additional Information: full citation, abstract, referenc

> A number of current technologies allow for the determination of interatomic dist
> proteins and RNA. Thus, the reconstruction of a three-dimensional set of points
> distances has become a task of basic importance in determining molecular struc
> obtains from techniques such as NMR are typically sparse and error-prone, grea
> Many of these errors re ...

> Keywords: biomolecular structure, distance geometry, random sampling, randor

70 Collision detection for deforming necklaces

Leonidas Guibas, An Nguyen, Daniel Russel, Li Zhang

June 2002   Proceedings of the eighteenth annual symposium on Computational ç

Full text available: pdf(571.15 KB)   Additional Information: full citation, abstract, references,

In this paper, we propose to study deformable necklaces --- flexible chains of bɛ
balls may intersect. Such objects can be used to model macro-molecules, muscl
physical world. In this paper, we exploit this linearity to develop geometric struc
useful in physical simulations. We show how these structures can be implementɛ
necklace deformatio ...

Keywords: bounding volume hierarchy, collision detection, deformable chains, p

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Shihhsien S. Kuo, Michael D. Altman, Jaydeep P. Bardhan, Bruce Tidor, Jacob K. W

November 2002   Proceedings of the 2002 IEEE/ACM international conference on Cɛ

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Computer simulation is an important tool for improving our understanding of biɛ
drug design. However, the numerical techniques used in these simulation tools ɛ
widely used in analyzing integrated circuit interconnects. In this paper we descri
analyze biomolecule electrostatics, present an integral formulation of the proble
method to accelerate the solut ...

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Boris A. Reva, Alexei V. Finkelstein, Jeffrey Skolnick

March 1998   Proceedings of the second annual international conference on Computɛ

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73 I/O limitations in parallel molecular dynamics

Terry W. Clark, L. Ridgway Scott, Stanislaw Wlodek, J. Andrew McCammon

December 1995 Proceedings of the 1995 ACM/IEEE conference on Supercomputing (

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74 A hierarchical load-balancing framework for dynamic multithreaded comput

Vijay Karamcheti, Andrew A. Chien

November 1998   Proceedings of the 1998 ACM/IEEE conference on Supercompul

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increasingly popular for expressing irregular applications based on sophisticated
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challenges, particularly with respect to load-balancing. Load-balancing technique
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Pierluigi Crescenzi, Deborah Goldman, Christos Papadimitriou, Antonio Piccolboni, |

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Michael Conrad

May 1985   Communications of the ACM, Volume 28 Issue 5

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more efficient systems for such applications as pattern recognition and process

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Yong L. Xiao, Donald E. Williams

April 1994   Proceedings of the 1994 ACM symposium on Applied computing

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Keywords: function optimization, genetic algorithms, intermolecular interctions,

79 Incorporating bioinformatics in an algorithms course

Lawrence D'Antonio

June 2003 ACM SIGCSE Bulletin , Proceedings of the 8th annual conference on Inno science education, Volume 35 Issue 3

Full text available: pdf(342.73 KB)   Additional Information: full citation, abstract, referen

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Keywords: bioinformatics, dynamic programming, palindromes, sequence alignn common superstring problem

80 Special issue on on inductive logic programming: llp: a short look back and

David Page, Ashwin Srinivasan

December 2003   The Journal of Machine Learning Research, Volume 4

Full text available: pdf(103.21 KB)   Additional Information: full citation,

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... y,bd[last].y)); if((idx==0)&&(idy==0)&&(next!=last)){ /* **overlap** , need to ....]j[0];
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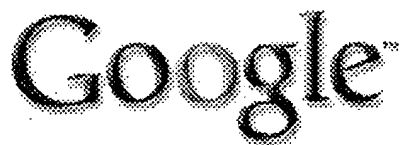
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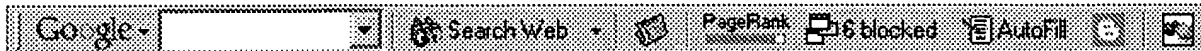www.lifesep.com/documents/HGMSjournal.pdf - Similar pages

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